

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 13:16:16 ON 14 AUG 2003

=> file medline biosis caplus
COST IN U.S. DOLLARS

| SINCE FILE ENTRY | TOTAL SESSION |
|---------------------|------------------|
| 0.21 | 0.21 |

FULL ESTIMATED COST

FILE 'MEDLINE' ENTERED AT 13:16:33 ON 14 AUG 2003

FILE 'BIOSIS' ENTERED AT 13:16:33 ON 14 AUG 2003
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FILE 'CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003
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=> g protein-coupled receptor
L1 25886 G PROTEIN-COUPLED RECEPTOR

=> polynucleotide
L2 33502 POLYNUCLEOTIDE

=> nucleic acid
L3 351190 NUCLEIC ACID

=> l2 or l3
L4 374190 L2 OR L3

=> l1 and l4
L5 1103 L1 AND L4

=> l5 and 1970-2000/py
2 FILES SEARCHED...
L6 457 L5 AND 1970-2000/PY

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)

=> peter?/au and lind?/au
L8 1192 PETER?/AU AND LIND?/AU

=> linda?/au and wood?/au
L9 93 LINDA?/AU AND WOOD?/AU

=> luis?/au and parodi?/au
L10 2 LUIS?/AU AND PARODI?/AU

=> gabriel?/au and vogeli?/au
L11 0 GABRIEL?/AU AND VOGELI?/AU

=> l8 or l9 or l10
L12 1287 L8 OR L9 OR L10

=> l7 and l12
L13 0 L7 AND L12

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003

BEST AVAILABLE COPY

L1 25886 G PROTEIN-COUPLED RECEPTOR
L2 33502 POLYNUCLEOTIDE
L3 351190 NUCLEIC ACID
L4 374190 L2 OR L3
L5 1103 L1 AND L4
L6 457 L5 AND 1970-2000/PY
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)
L8 1192 PETER?/AU AND LIND?/AU
L9 93 LINDA?/AU AND WOOD?/AU
L10 2 LUIS?/AU AND PARODI?/AU
L11 0 GABRIEL?/AU AND VOGELI?/AU
L12 1287 L8 OR L9 OR L10
L13 0 L7 AND L12

=> logoff

Sequence Comparison A

US-09-884-430-3

; Sequence 3, Application US/09884430
 ; Patent No. US20020151046A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Santiago, Immaculada Silos
 ; TITLE OF INVENTION: 52871, A NOVEL HUMAN G PROTEIN COUPLED
 ; TITLE OF INVENTION: RECEPTOR AND USES THEREOF
 ; FILE REFERENCE: MNI-165
 ; CURRENT APPLICATION NUMBER: US/09/884,430
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: USSN 60/212,331
 ; PRIOR FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: USSN 60/269,758
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1044
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1044)

US-09-884-430-3

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1.04e-195 | Length: | 1044 |
| Score: | 1757.00 | Matches: | 337 |
| Percent Similarity: | 98.83% | Conservative: | 1 |
| Best Local Similarity: | 98.54% | Mismatches: | 4 |
| Query Match: | 90.80% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-09-750-373-25 (1-371) x US-09-884-430-3 (1-1044)

| | | | |
|----|-----|---|-----|
| Qy | 1 | MetProAlaAsnPheThrGluGlySerPheAspSerSerGlyThrGlyGlnThrLeuAsp | 20 |
| Db | 1 | ATGCCAGCCAACCTTCACAGAGGGCAGCTTCGATTCCAGTGGGACCGGGCAGACGCTGGAT | 60 |
| Qy | 21 | SerSerProValAlaCysThrGluThrValThrPheThrGluValValGluGlyLysGlu | 40 |
| Db | 61 | TCTTCCCCAGTGGCTTGCACTGAAGCAGTGACTTTTACTGAAGTGGTGAAAGGAAAGGAA | 120 |
| Qy | 41 | TrpGlySerPheTyrTyrSerPheLysThrGluGlnLeuIleThrLeuTrpValLeuPhe | 60 |
| Db | 121 | TGGGGTTCCTTCTACTACTCCTTTAAGACTGAGCAATTGATAACTCTGTGGGTCCTCTTT | 180 |
| Qy | 61 | ValPheThrIleValGlyAsnSerValValLeuPheSerThrTrpArgArgLysLysLys | 80 |
| Db | 181 | GTTTTTACCATTGTTGGAACTCCGTTGTGCTTTTTTCCACATGGAGGAGAAAGAAGAAG | 240 |
| Qy | 81 | SerArgMetThrPhePheValThrGlnLeuAlaIleThrAspSerPheThrGlyLeuVal | 100 |
| Db | 241 | TCAAGAATGACCTTCTTTGTGACTCAGCTGGCCATCACAGATTCTTTCACAGGACTGGTC | 300 |

| | | | |
|----|------|--|------|
| Qy | 101 | AsnIleLeuThrAspIleIleTrpArgPheThrGlyAspPheThrAlaProAspLeuVal | 120 |
| Db | 301 | | |
| Qy | 121 | CysArgValValArgTyrLeuGlnValValLeuLeuTyrAlaSerThrTyrValLeuVal | 140 |
| Db | 361 | | |
| Qy | 141 | SerLeuSerIleAspArgTyrHisAlaIleValTyrProMetLysPheLeuGlnGlyGlu | 160 |
| Db | 421 | | |
| Qy | 161 | LysGlnAlaArgValLeuIleValIleAlaTrpSerLeuSerPheLeuPheSerIlePro | 180 |
| Db | 481 | | |
| Qy | 181 | ThrLeuIleIlePheGlyLysArgThrLeuSerAsnGlyGluValGlnCysTrpAlaLeu | 200 |
| Db | 541 | | |
| Qy | 201 | TrpProGlyAspSerTyrTrpThrProTyrMetThrIleValAlaPheLeuValTyrPhe | 220 |
| Db | 601 | | |
| Qy | 221 | IleProLeuThrIleIleSerIleMetTyrGlyIleValIleArgThrIleTrpIleLys | 240 |
| Db | 661 | | |
| Qy | 241 | SerLysThrTyrGluThrValIleSerAsnCysSerAspGlyLysLeuCysSerSerTyr | 260 |
| Db | 721 | | |
| Qy | 261 | AsnArgGlyLeuIleSerLysAlaLysIleLysAlaIleLysTyrSerIleIleIleIle | 280 |
| Db | 781 | | |
| Qy | 281 | LeuAlaPheIleCysCysTrpSerProTyrPheLeuPheAspIleLeuAspAsnPheAsn | 300 |
| Db | 841 | | |
| Qy | 301 | LeuLeuProAspThrGlnGluArgPheTyrAlaSerValIleIleGlnAsnLeuProAla | 320 |
| Db | 901 | | |
| Qy | 321 | LeuAsnSerAlaIleAsnProProIleTyrCysValPheSerSerSerIleSerPhePro | 340 |
| Db | 961 | | |
| Qy | 341 | CysArg | 342 |
| Db | 1021 | | |
| Qy | 361 | TGCAGG | 1026 |

Sequence Comparison B

LOCUS AI500347 414 bp mRNA linear EST 14-APR-1999
 DEFINITION tm95f03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165885
 3',
 mRNA sequence.
 ACCESSION AI500347
 VERSION AI500347.1 GI:4392329
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
 M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing
 Center
 Clone distribution: NCI-CGAP clone distribution information can
 be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1403 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 399.
 FEATURES Location/Qualifiers
 source 1. .414
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2165885"
 /clone_lib="NCI_CGAP_Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT7T3D-Pac
 (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco
 RI; 1st
 strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and
 cloned into
 the Not I and Eco RI sites of the modified pT7T3
 vector.
 Library is normalized, and was constructed by
 Bento

| | | | | |
|------------|------|------|-------|-------|
| BASE COUNT | 86 a | 96 c | 129 g | 103 t |
| ORIGIN | | | | |

| | | | |
|----|------|--|------|
| Qy | 1206 | CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTAGACCCTAGGGCAGTGCCAGTGC | 1265 |
| | | | |
| Db | 414 | CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTTAGACCCTAGGGCAGTGCCAGTGC | 355 |
| | | | |
| Qy | 1266 | TAGGCTGAGCACCATCAGCTCTCCCAGGTCCTTGTCACCTGCTTGGGCACGTGCATGGAA | 1325 |
| | | | |
| Db | 354 | TAGGCTGAGCACCATCAGCTCTCCCAGGTCCTTGTCACCTGCTTGGGCACGTGCATGGAA | 295 |
| | | | |
| Qy | 1326 | CCCAGCCAACTTCACCCCCACCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT | 1385 |
| | | | |
| Db | 294 | CCCAGCCACTCACCCCCACCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT | 235 |
| | | | |
| Qy | 1386 | AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCAGTTATTTCATGCCAG | 1445 |
| | | | |
| Db | 234 | AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCAGTTATTTCATGCCAG | 175 |
| | | | |
| Qy | 1446 | CCAGGAAGGAAAACGCCCTTCCCTTCCCCACCATTTCCAGCCCTCCTTCCCCTGGCCAGCAC | 1505 |
| | | | |
| Db | 174 | CCAGGAAGGAAAACGCC - TCCTTCCCCACCATTTCCAGCCCTCCTTCCCCTGGCCAGCAC | 116 |
| | | | |
| Qy | 1506 | CTGAACCCAGTGAACACAGGCATTAGTGGTCCAGGGTCCTGGCTTGGAGCCAGTGAGTAG | 1565 |
| | | | |
| Db | 115 | CTGAACCCAGTGAACACAGGCATCAGTGGTCCAGGGTCCTGGCTTGGAGCCAGTGAGTAG | 56 |
| | | | |
| Qy | 1566 | ACAGGCAAGCAGAGGGGACAAAAGGTAGCTGGGGTTATACATGAATATTCTCATTAC | 1620 |
| | | | |
| Db | 55 | ACAGGCAAGCAGAGGGGACAAAAGGTAGCTGGGGTTATACATGAATATTCTCATTAC | 1 |

WEST Search History

DATE: Thursday, August 14, 2003

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=AND

| | | | |
|-----|--|-------|-----|
| L12 | l6 and L11 | 0 | L12 |
| L11 | l7 or l8 or l9 | 42 | L11 |
| L10 | gabriel.in. and vogeli.in. | 0 | L10 |
| L9 | luis.in. and parodi.in. | 3 | L9 |
| L8 | linda.in. and wood.in. | 17 | L8 |
| L7 | peter.in. and lind.in. | 22 | L7 |
| L6 | L5 and isolated | 1038 | L6 |
| L5 | l1 and L4 | 1098 | L5 |
| L4 | l2 or L3 | 48153 | L4 |
| L3 | nucleic adj acid | 46574 | L3 |
| L2 | polynucleotide | 17758 | L2 |
| L1 | g adj protein adj coupled adj receptor | 1594 | L1 |

END OF SEARCH HISTORY